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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=14; hr=18; min=42; sec=41; ms=906;]

=====

Reviewer Comments:

<210> 3
<211> 951
<212> DNA
<213> Mouse

Per 1.823 of the Sequence Rules, the only valid <213> responses are:
the Genus species of the organism, "Artificial Sequence," or "Unknown."
"Artificial Sequence" and "Unknown" require explanation in the <220>-
<223> section. Please give the Genus species. This response appears in
subsequent sequences.

<210> 9
<211> 1670
<212> DNA
<213> Chimera

The above <213> response is invalid: since this is a chimeric sequence,
please use "Artificial Sequence," and give the sources in the <220>-
<223> section. Same response in subsequent sequences.

Application No: 10824481

Version No: 2.0

Input Set:

Output Set:

Started: 2008-03-04 15:06:46.434

Finished: 2008-03-04 15:06:48.842

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 408 ms

Total Warnings: 30

Total Errors: 0

No. of SeqIDs Defined: 35

Actual SeqID Count: 35

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)

Input Set:

Output Set:

Started: 2008-03-04 15:06:46.434
Finished: 2008-03-04 15:06:48.842
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 408 ms
Total Warnings: 30
Total Errors: 0
No. of SeqIDs Defined: 35
Actual SeqID Count: 35

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Wyeth
Ling, Vincent
Carreno, Beatriz M.
Collins, Mary

<120> USE OF B7-H3 TO INHIBIT LYMPHOCYTE PROLIFERATION (As Amended)

<130> 08702.6108-00000

<140> 10824481

<141> 2004-04-15

<160> 35

<170> PatentIn version 3.5

<210> 1

<211> 951

<212> DNA

<213> Homo sapiens

<400> 1

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ctggtgggca ccatgccac cctgtgtgc tccttctccc ctgagcctgg cttcagcctg	180
gcacagctca acctcatctg gcagctgaca gataccaaac agctgggtgca cagctttgct	240
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gcacagggca acgcatcct gaggtctcag cgcgtgcgtg tggcggacga gggcagcttc	360
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gtgaccatca cgtgtccag ctaccggggc taacctgagg ctgagggtt ctggcaggat	540
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ttgtttgatg tgacacagct cctgcgggtg gtgtgggtg cgaatggcac ctacagctgc	660
ctggtgcgca acccgtgct gcagcaggat gcgcacggct ctgtcaccat cacagggcag	720
cctatgacat tccccccaga ggcctgttg gtgacctgg ggctgtctgt ctgtctcatt	780
gcaetgctgg tggccctggc ttctgtgtgc tggagaaaga tcaaacagag ctgtgaggag	840
gagaatgcag gagctgagga ccaggatggg gagggagaag gctccaagac agcctgcag	900
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<210> 2

<211> 316

<212> PRT

<213> Homo sapiens

<400> 2

Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly Ala
1 5 10 15

Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln
20 25 30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
 210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln
 225 230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser
 245 250 255

Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg
 260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln
 275 280 285

Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro Leu Lys His
 290 295 300

Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala
 305 310 315

<210> 3

<211> 951

<212> DNA

<213> Mouse

<400> 3

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ctgtgggaca cggatgccac cctacgtgc tcctttccc cagagcctgg ctacgtctg 180

gcacagctca acctcatctg gcagctgaca gacacaaac agctgggtgca cagcttcacg 240

gagggccggg accaaggcag tgcctactcc aaccgcacag cgtcttccc tgacctgttg 300

gtgcaaggca atgcgtcctt gaggtgcag cgcgtccgag taaccgacga ggagcgtac 360

acctgctttg tgagcattca ggaatttgac agcgtgtgtg ttacgtgtgca ggtggccgcc 420

cctactcga agcccagcat gacctggag cccaacaagg acctacgtcc agggaaacatg 480

gtgaccatca cgtgtctctg ctaccagggc tatccggagg ccgaggtgtt ctggaaggat 540

ggacaggagg tgcccttgac tggcaatgtg accacatccc agatggccaa cgagcggggc 600

ttgttcgatg ttcacagcgt gctgaggggtg gtgctgggtg ctaacggcac ctacagctgc	660
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ccctgacat tccccctga ggcctctgtg gtaaccgtgg ggcctctctgt ctgtcttctg	780
gtactactgg tggccctggc ttctgtgtgc tggagaaaga tcaagcagag ctgcgaggag	840
gagaatgcag gtgccgagga ccaggatgga gatggagaag gatccaagac agctctacgg	900
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<210> 4

<211> 316

<212> PRT

<213> Mouse

<400> 4

Met	Leu	Arg	Gly	Trp	Gly	Gly	Pro	Ser	Val	Gly	Val	Cys	Val	Arg	Thr
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Ala	Leu	Gly	Val	Leu	Cys	Leu	Cys	Leu	Thr	Gly	Ala	Val	Glu	Val	Gln
			20						25					30	

Val	Ser	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Asp	Thr	Asp	Ala	Thr	Leu
		35						40				45			

Arg	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn
	50						55						60		

Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Thr
65					70				75						80

Glu	Gly	Arg	Asp	Gln	Gly	Ser	Ala	Tyr	Ser	Asn	Arg	Thr	Ala	Leu	Phe
				85						90				95	

Pro	Asp	Leu	Leu	Val	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	Val
			100					105						110	

Arg	Val	Thr	Asp	Glu	Gly	Ser	Tyr	Thr	Cys	Phe	Val	Ser	Ile	Gln	Asp
		115						120						125	

Phe	Asp	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys
	130							135						140	

Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asn	Met
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Lys Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Arg Gly Leu Phe Asp Val His Ser Val Leu
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln
225 230 235 240

Pro Leu Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser
245 250 255

Val Cys Leu Val Val Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg
260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln
275 280 285

Asp Gly Asp Gly Glu Gly Ser Lys Thr Ala Leu Arg Pro Leu Lys Pro
290 295 300

Ser Glu Asn Lys Glu Asp Asp Gly Gln Glu Ile Ala
305 310 315

<210> 5

<211> 1605

<212> DNA

<213> Homo sapiens

<400> 5

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ctgtggggca cegatgccac cctgtgetgc tcttctctc ctgagcctgg cttcagcctg 180

gcacagctca acctcatctg gcagctgaca gataccaaac agctgggtgca cagctttgtc 240

gagggccagg accagggcag cgcctatgcc aaccgcacgg cccctctccc ggacctgctg	300
gcacagggca acgcacccct gaggtgcag cgcgtgcgtg tggcggacga gggcagcttc	360
acctgcttcg tgagcatccg ggaatttcggc agcgtgcgcg tcagcctgca ggtggcgcgt	420
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gtgaccatca cgtgctccag ctaccagggc taccctgagg ctgagggtgtt ctggcaggat	540
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ctggtgcgca accccgtgct gcagcaggat gcgcacagct gtgtcaccat cacacccacg	720
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gcaggagctg aggaccagga tggggaggga gaaggctcca agacagccct gcagcctctg	1560
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<210> 6

<211> 534

<212> PRT

<213> Homo sapiens

<400> 6

Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly Ala

1

5

10

15

Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln
 20 25 30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
 35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
 50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
 65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
 85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
 100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
 115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
 130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
 145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
 165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
 180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu
 195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
 210 215 220

Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln
 225 230 235 240

Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val
245 250 255

Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro
260 265 270

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr
275 280 285

Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly
290 295 300

Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln
305 310 315 320

Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly
325 330 335

Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val
340 345 350

Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
355 360 365

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser
370 375 380

Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln
385 390 395 400

Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu
405 410 415

Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala
420 425 430

Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp
435 440 445

Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro
450 455 460

Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu

465

470

475

480

Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys
 485 490 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly
 500 505 510

Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp
 515 520 525

Asp Gly Gln Glu Ile Ala
 530

<210> 7

<211> 112

<212> PRT

<213> Homo sapiens

<400> 7

Ala Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly
 1 5 10 15

Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser
 20 25 30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu
 35 40 45

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn
 50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu
 65 70 75 80

Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe
 85 90 95

Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala
 100 105 110

<210> 8

<211> 112

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> L, or V, or any other amino acid

<220>

<221> MISC_FEATURE

<222> (22)..(22)

<223> C, or R, or any other amino acid

<220>

<221> MISC_FEATURE

<222> (53)..(53)

<223> A, or T, or any other amino acid

<220>

<221> MISC_FEATURE

<222> (56)..(56)

<223> Q, or R, or any other amino acid

<400> 8

Ala Xaa Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly
1 5 10 15

Thr Asp Ala Thr Leu Xaa Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser
20 25 30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu
35 40 45

Val His Ser Phe Xaa Glu Gly Xaa Asp Gln Gly Ser Ala Tyr Ala Asn
50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu
65 70 75 80

Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe
85 90 95

Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala
100 105 110

<210> 9

<211> 1670

<212> DNA

<213> Chimera

<400> 9

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